CLAIMS

1. A process for detecting chromosomal overrepresentation in cells, comprising the following steps:

(a) isolating DNAs from cells which have no known numerical changes in their DNAs, and amplifying the DNAs by means of a PCR method using tag primers;

(b) hybridizing cells under study *in situ* with the amplified DNAs from (a);

(c) amplifying DNAs from the *in situ* hybridized cells from (b) by means of a PCR method using the tag primers from (a);

(d) cohybridizing the DNAs from (a) and (c) to metaphase chromosome spreads from normal cells under suppression hybridization conditions; and

(e) identifying numerical changes in the amplified DNAs from (c).

2. The process according to claim 1, wherein the cells under study originate from tumors.

3. The process according to claim 1, wherein the cells under study originate from the blood of pregnant persons.

4. The process according to claim 2 or 3, wherein the cells under study are those of a cell population or single cells.

5. The process according to claim 1, wherein the cells under study have an interphase nucleus.

6. The process according to claim 1, wherein the tag primers are degenerative primers.

7 The process according to claim 1, wherein the identification from (d) comprises a "Comparative Genomic Hybridization" (CGH) method.

8. A kit for carrying out the process according to claim 1, comprising the following components: